

GenCore version 5.1.3
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29: em_vi: *
30: em_htq_hum: *
31: em_htq_inv: *
32: em_htq_other: *

4 protein - nucleic search, using frame plus 820 model

on: January 16, 2003, 16:55:57 ; Search time 10:56.51 Seconds
(without alignments) ; 340,553 Main alignments ; 340,553 Main words ; 340,553 Main characters

title: US-09-856-070-21
perfect score: 60
Sequence: 1 EELMLRLQDYEE 12

Scoring table: **HISUMG2**

Scoring table:	Xgapop	Ygapop	Xgapext	Ygapext	0.5
Xgapop	10.0				0.5
Ygapop	10.0				0.5
Xgapext			10.0		0.5
Ygapext			10.0		0.5
Fgapop	6.0				7.0
Fgapext			6.0		7.0
Delop				6.0	7.0
Delext				6.0	7.0

maximum DB seq. length: 200000000

database:

24	44	73.3	177263	8	A0003376	Oryza sativa
25	44	73.3	187415	2	A011226	Homo sapiens
26	44	73.3	187981	2	A0113786	Homo sapiens
27	42	70.0	182796	2	A0034891	Oryza sativa
28	42	70.0	184149	2	A0005053	Oryza sativa
29	42	70.0	232339	9	A0007446	A0767456
30	41	68.3	63650	2	A0109211	Mus musculus
31	41	68.3	71132	2	A0003840	Oryza sativa
32	41	68.3	138822	5	A0091041	Gallus gallus
33	41	68.3	143764	8	A0004305	Oryza sativa
34	41	68.3	145659	2	A0114942	Rattus norvegicus
35	41	68.3	160047	9	A1357935	Human DNA
36	41	68.3	173775	2	A0799433	Trypanosoma brucei
37	41	68.3	231285	2	A0025125	Oryza sativa
38	41	68.3	262238	1	A0115703	Mus musculus
39	40	66.7	343	8	YSAAK2B	Candida malayana
40	41	66.7	1084	1	MMU28498	Barrelia hirsutissima
41	40	66.7	5902	5	A0325322	A075130
42	40	66.7	105796	2	A0099130	Rattus norvegicus
43	40	66.7	107762	2	A0004141	Oryza sativa
44	40	66.7	118376	2	A0004180	Oryza sativa
45	40	66.7	126645	2	A0734616	Oryza sativa

ALIGNMENT

RESULT 1

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation distinction may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry, or covered by high quality data (i.e., fitted quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TRIMBL; Wp, WORMPEP; information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/wormpep/>; this sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/CGP/chrc6/>.

RP11-507C10 is from the library KIC; 11.2 constructed by the group of Piotter de Jong. For further details see <http://www.chr6.sanger.ac.uk/>. VECTOR: place3,6

This sequence is the entire insert of clone RP11-507C10. The true right end of clone RP11-507C10 is at 47323 in this sequence. Location/Qualifiers

1.. 215705
/organism="Homo sapiens"
/db_xref="EntrezGene:6026"
/chromosome="6"
/map="q25;2-26"
/clone="RP11-507C10"
/clone_id="RP11-507C10" 2.. 37002..37057

/note="Single clone region. Sequence from reads from a short insert library derived from a single PUC clone. Restriction digest data confirm the assembly." 156422..156454

/note="Sequence from unidirectional primer reads only." 156427..156427

unsure 572297 a .. 50282 ~ 49124 3 59002 t
BASE COUNT

ORIGIN

FEATURES

Source

misc_feature

Alignment Scores:		Length:	
Printed No.:	0.00654	Matches:	475
Score:	55.00	Conservative:	11
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	91.67%	Gaps:	0
DB:	9		

OS: 0.9 - 0.6 · 0.70 · 2.1 (1-12) × AF118897 (1-475)

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Search completed: January 16, 2003, 19:04:48